



SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> P04885US1

<140> 09/833,017

<141> 2001-04-10

<150> PCT/CA00/00605

<151> 2000-05-25

<150> 2,302,861

<151> 2000-04-10

<150> 2,332,733

<151> 2001-02-20

<160> 28

<170> PatentIn version 3.0

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<212> DNA

<213> Streptococcus mutans

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<221> CDS

<222> (1)..(141)

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1 5 10 15  
gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96  
Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30  
ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141  
Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

<210> 2

<211> 46

<212> PRT

<213> Streptococcus mutans

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<211> 1326

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1 5 10 15

acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96  
Thr Val Leu Phe Leu Leu Phe Leu Ser Lys Val Ser Asn Val Thr  
20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144  
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile  
35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192  
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu  
50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser			
65	70	75	80
ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac			288
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp			
85	90	95	
ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga			336
Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly			
100	105	110	
att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca			384
Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala			
115	120	125	
gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att			432
Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile			
130	135	140	
ggc cga ctt aaa gat agt ttg acc aag atg aag gtc aaa aaa cgc ttg			480
Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu			
145	150	155	160
att cca atg aat att act atg ctt cta tac tac ctt tta ata cag gta			528
Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val			
165	170	175	
ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt			576
Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg			
180	185	190	
aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca			624
Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser			
195	200	205	
ttt tta agc caa tat acc aaa caa aag gtt caa aat gag ata atg gca			672
Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala			
210	215	220	
caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata			720
Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile			
225	230	235	240
gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat			768
Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn			
245	250	255	
att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt			816
Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser			
260	265	270	
att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg			864
Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu			
275	280	285	
cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat			912
Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp			

290	295	300	
gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys			
305	310	315	960
320			
aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu			
325	330	335	1008
atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn			
340	345	350	1056
gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala			
355	360	365	1104
ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr			
370	375	380	1152
aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser			
385	390	395	400
act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile			
405	410	415	1200
420			
ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His			
425	430		1248
430			
tta ttc aag caa ctc cta ata ata aaa tag Leu Phe Lys Gln Leu Leu Ile Ile Lys			
435	440		1296
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<213> Streptococcus mutans			
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Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu			
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Thr Val Leu Phe Leu Leu Phe Ser Lys Val Ser Asn Val Thr			
20	25	30	

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile  
35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu  
50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser  
65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp  
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly  
100 105 110

Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala  
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile  
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu  
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val  
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg  
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser  
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala  
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile  
225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn  
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser  
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu  
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp  
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys  
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu  
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn  
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala  
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr  
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser  
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile  
405 410 415

Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His  
420 425 430

Leu Phe Lys Gln Leu Leu Ile Ile Lys  
435 440

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205			
gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg	210	215	672
220			
aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg	225	230	720
235			
240			
gct gtg att gct gat caa agg aga gca aaa Ala Val Ile Ala Asp Gln Arg Arg Ala Lys	245	250	750
<210> 6			
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Met Ile Ser Ile Phe Val Leu Glu Asp Asp Phe Leu Gln Gln Gly Arg 1 5 10 15			
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr 20 25 30			
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile 35 40 45			
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys 50 55 60			
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His 65 70 75 80			
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met 85 90 95			
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys 100 105 110			

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr  
115                    120                    125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe  
130                    135                    140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile  
145                    150                    155                    160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr  
165                    170                    175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys  
180                    185                    190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro  
195                    200                    205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg  
210                    215                    220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg  
225                    230                    235                    240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys  
245                    250

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<212> PRT

<213> Streptococcus mutans

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<221> PEPTIDE

<222> (1)..(46)

<400> 7

Met Lys Lys Thr Pro Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

<210> 8

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<213> Streptococcus mutans

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<222> (1)..(46)

<400> 8

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

<210> 9

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<222> (1)..(46)

<400> 9

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<222> (1)..(43)

<400> 10

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala  
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<400> 11

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<222> (1)..(46)

<400> 12

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr  
1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

<210> 13

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<213> Streptococcus mutans

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<400> 13

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1 5 10 15

Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe  
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys  
35 40 45

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<213> synthetic construct

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<222> (1)..(21)

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Gln Ala Leu Gly Lys  
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<211> 19

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<221> STS

<222> (1)..(19)

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<222> (1)..(20)

<400> 16  
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<400> 17  
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21

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21

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22

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<212> DNA  
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<220>

<221> misc\_feature  
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aaaaaaaaatgac tttaaagaaaa ttaagactga tgaatttagag attatcatttgcgg 180  
aaggcttatca acatttttcc ggctgtttaa cagaagttt acacaagctt tggaaaata 240  
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aaaataaaaaa tacagggtta aataatcaag tgtgctgtcg tggatgagaa gataaaacta 360  
tctcttagag aataggcctc ctctatttttta ttatttaggat ttgcttgaat aaatgtatgt 420  
gattgcttgtt ttgtaaaactg gttttggat aatgttcaag aatatgatttcc acctttgcta 480  
aaccaataacc gcgattggag ccttttagtgg aatagtttc tttaaaaattttaactcacat 540  
ctatttgttt ttctttgggtg gaattctgaa tgataaagac tatactgccat tttttcttaa 600  
aaaaggctaa ctgaatttca ggatttaatg attcgaaagc agcctcaatg gcattatcac 660  
acaagataga aagtatggta atgaaatcaa gcaactccat ctcaggcagt tgtattttac 720  
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ttaaagtccg	tatcacatta	taactctcta	taacatacaa	tacctgtatt	aaaaggtagt	1200
atagaagcat	agtaatattc	attggaatca	agcgaaaa	gacccatc	ttggtaaac	1260
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tccaaaaata	gtcaattctt	tataagacca	attttttct	ttcatgatag	ctgcaatgg	2400
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acgatatcac	tcaataaaat	ctactaactt	aataacc			2557

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<211> 480

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)...(408)

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Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val		
1 5 10 15		
tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat	96	
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp		
20 25 30		
tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat	144	
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His		
35 40 45		
cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca	192	
Pro Glu Leu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr		
50 55 60		
cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag	240	
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln		
65 70 75 80		
aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa	288	
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu		
85 90 95		
cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt	336	
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe		
100 105 110		
cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa	384	
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln		
115 120 125		
gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaaag gcaaagtatg	438	
Glu Leu Phe Glu Arg Leu Val Ala		
130 135		
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<210> 23

<211> 136

<212> PRT

<213> Streptococcus mutans

<400> 23

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Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp  
20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His  
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr  
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln  
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu  
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe  
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln  
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala  
130 135

<210> 24

<211> 680

<212> DNA

<213> Streptococcus mutans

<220>

<221> misc\_feature

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 tttataataa ttttattata aaaggaggc atcgtaatag atggaagaag attttcaa 120  
 tgtttttaat aaggtaagc caattgtatg gaaatthaagc cgtttattact ttatcaa 180  
 gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240  
 acatccagaa ttagaagagg atgatacataa attgtatatac tatttaaga cacgttttc 300  
 taattacatt aaagatgtt tgcgtcagca agaaagtca aacgtcgtt ttaatagaat 360  
 gtcttatgaa gaagtccgtg agattgaaca ctgttgtca agtggcggtt tgcaattgga 420  
 tgaatatatt ttatcggt atagtttgct tgcataaaaa caaggctcgt gtactgaaaa 480  
 gcaagagctg tttgagcgct tggtagcagg agagcactt ttggaaaggc aaagtatgct 540  
 gaaagattta cgtaaaaaat taagtgatt taaggaaaa tagttaaaaa gggaaagaat 600  
 ggaacatgtg attgtaccat tcttttggt tgaaaattaa gaaaagttat tataaattat 660  
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<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(2280)

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 Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile  
 1 5 10 15  
 ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96  
 Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser  
 20 25 30  
 tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144  
 Ser Ser Asn Pro Leu Pro Asp Gln Ser Lys Leu Phe Trp Arg Arg

35	40	45	
cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala			192
50	55	60	
gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala			240
65	70	75	80
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tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu			288
85	90	95	
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile			336
100	105	110	
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe			384
115	120	125	
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val			432
130	135	140	
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser			480
145	150	155	160
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr			528
165	170	175	
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys			576
180	185	190	
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln			624
195	200	205	
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc Lys Ala Leu Met Thr Tyr Ile Ile Ala Ser Leu Ile Val Thr Leu			672
210	215	220	
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr			720
225	230	235	240
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu			768
245	250	255	
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr			816
260	265	270	

ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser	275	280	285	864
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tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg	290	295	300	912
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cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile	305	310	315	960
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gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met	325	330	335	1008
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gta att ttg gtt ggt ggg gtt ttg gcg caa aac aat aac ctt ttc Val Ile Leu Val Gly Gly Val Leu Ala Gln Asn Asn Asn Leu Phe	340	345	350	1056
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ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala	355	360	365	1104
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ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn	370	375	380	1152
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gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc Ala Val Val Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr	385	390	395	1200
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att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser	405	410	415	1248
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gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser	420	425	430	1296
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gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val	435	440	445	1344
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gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser	450	455	460	1392
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gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn	465	470	475	1440
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cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg	485	490	495	1488

gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe 500 505 510	1536
gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile 515 520 525	1584
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu 530 535 540	1632
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545 550 555 560	1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565 570 575	1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580 585 590	1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595 600 605	1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610 615 620	1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625 630 635 640	1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645 650 655	1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660 665 670	2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675 680 685	2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690 695 700	2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705 710 715 720	2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag	2208

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln  
725 730 735

gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa 2256  
Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln  
740 745 750

ggt ttc tat tat aac ctg ttt aat 2280  
Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile  
1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser  
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg  
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala  
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala  
65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu  
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile  
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe  
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val

130

135

140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser  
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr  
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys  
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln  
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu  
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr  
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu  
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr  
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser  
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg  
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile  
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met  
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe  
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala  
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn  
370                   375                   380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr  
385                   390                   395                   400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser  
405                   410                   415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser  
420                   425                   430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val  
435                   440                   445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser  
450                   455                   460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn  
465                   470                   475                   480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg  
485                   490                   495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe  
500                   505                   510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile  
515                   520                   525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu  
530                   535                   540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val  
545                   550                   555                   560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn  
565                   570                   575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu  
580                   585                   590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro  
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu  
610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu  
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln  
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg  
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu  
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile  
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His  
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln  
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln  
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn  
755 760

<210> 27

<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(900)

<400> 27

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cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc 96  
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile  
20 25 30

ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att 144  
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile  
35 40 45

tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct 192  
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser  
50 55 60

tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct 240  
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala  
65 70 75 80

gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca 288  
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro  
85 90 95

aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga 336  
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg  
100 105 110

gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag 384  
Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys  
115 120 125

tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac 432  
Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp  
130 135 140

aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att 480  
Lys Glu Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile  
145 150 155 160

ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt 528  
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly  
165 170 175

gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat 576  
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp  
180 185 190

att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat 624  
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp

195	200	205	
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu 210                   215                   220			672
aaa aag gga aat gac aag gtt att gaa gga aaa att aac aat gtc Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val 225                   230                   235                   240			720
gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr 245                   250                   255			768
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly 260                   265                   270			816
atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp 275                   280                   285			864
tat ttc aaa gat aaa tta ctg cat aaa atg gat aat Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn 290                   295                   300			900
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<212> PRT			
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His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile 20                   25                   30			
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile 35                   40                   45			
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser 50                   55                   60			
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala 65                   70                   75                   80			

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro  
85 90 95

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg  
100 105 110

Glu Glu Lys Glu Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys  
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Ser Lys Asp  
130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile  
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly  
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp  
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp  
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu  
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val  
225 230 235 240

Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr  
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly  
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp  
275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn  
290 295 300